

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 27, 2003, 12:55:07 ; Search time 11.0695 Seconds

(without alignments)  
2585.358 Million cell updates/sec

Title: US-09-762-767a-2

Sequence: 1 MFCRLKDKITGECPSLL.....OKKVDGDNANFKASGID 690

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: SWISSPROT\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3593	100.0	690	1 CYG3_HUMAN	002108 homo sapien
2	3232	90.0	680	1 CYG3_RAT	P19686 ratu
3	3107	86.5	681	1 CYG3_BOVIN	P19687 bos tauru
4	1631	46.0	730	1 CYG4_RAT	Q9WY14 ratu
5	1631	45.0	732	1 CYG4_HUMAN	P33402 homo sapien
6	976.5	27.2	683	1 CYG1_DROME	Q07093 drosophila
7	795	22.1	619	1 CYG1_RAT	P20595 ratu
8	793.5	22.0	619	1 CYG1_BOVIN	P16068 bos tauru
9	789.5	22.0	619	1 CYG1_HUMAN	002153 homo sapien
10	774.5	21.6	682	1 CYG2_HUMAN	P22171 ratu
11	708	19.7	617	1 CYG2_BOVIN	075343 homo sapien
12	460	12.8	1047	1 ANPB_HUMAN	P46197 bos tauru
13	460	12.8	1047	1 ANPB_BOVIN	P05054 homo sapien
14	460	12.8	1047	1 ANPB_HUMAN	P16067 ratu
15	457.5	12.7	1057	1 ANPB_RAT	P18910 ratu
16	456.5	12.7	1061	1 ANPB_HUMAN	P16066 homo sapien
17	454.5	12.6	1057	1 ANPB_MOUSE	P18293 mus muscu
18	452	12.6	433	1 KSGC_RAT	P52785 ratu
19	450	12.5	1108	1 CYGE_MOUSE	P52785 mus muscu
20	448	12.5	1108	1 CYGE_RAT	P51840 ratu
21	445	12.4	1109	1 CYGD_CANFA	019191 canis fami
22	442	12.3	1108	1 CYGF_HUMAN	P19841 homo sapien
23	440	12.2	1103	1 CYGF_BOVIN	002740 bos tauru
24	438	12.2	1108	1 CYGF_RAT	P19842 ratu
25	438	12.2	1110	1 CYGD_BOVIN	P52203 bos tauru
26	434	12.1	1103	1 CYGD_HUMAN	002846 homo sapien
27	430	12.0	1110	1 CYC3_RAT	P51839 ratu
28	428.5	11.9	1050	1 ANPB_LANCA	P52202 anguilla ja
29	427	11.9	1135	1 CYGS_STRPD	P16065 strygnocoe
30	414.5	11.5	1073	1 HSER_PTIG	P35204 sus scrofa
31	408.5	11.4	1073	1 HSER_HUMAN	P25092 homo sapien
32	407.5	11.3	1072	1 HSER_RAT	P33897 ratu
33	399.5	11.1	1076	1 HSER_CAVDO	P70106 cavia porce

34	389	10.8	1137	1 CYG1_CAEEL	009435 caenorhabd
35	322.5	9.0	887	1 CYA2_HUMAN	008463 homo sapien
36	322	9.0	1068	1 CYA1_RAT	P26770 ratu
37	312.5	8.9	1059	1 CYA1_MOUSE	P26782 mus muscu
38	319	8.9	1090	1 CYA2_RAT	P26783 ratu
39	316	8.8	1080	1 CYA1_HUMAN	P26783 homo sapien
40	310.5	8.6	1078	1 CYA1_BOVIN	Q29450 bos tauru
41	303.5	8.4	1144	1 CYA3_HUMAN	050266 homo sapien
42	303	8.4	1144	1 CYA3_RAT	P21932 ratu
43	302	8.4	1134	1 CYA1_BOVIN	P19754 bos tauru
44	290.5	8.1	2248	1 CYA1_DROME	P32870 drosophila
45	287.5	8.0	1249	1 CYA8_MOUSE	P97490 mus muscu

## ALIGNMENTS

RESULT 1	CYG3_HUMAN	STANDARD:	PRT:	690 AA.
ID	CYG3_HUMAN	043843;		
AC	002108; 043843;			
DT	01-JUL-1993 (rel. 26, Created)			
DT	30-MAY-2000 (rel. 39, Last sequence update)			
DT	16-OCT-2001 (rel. 40, Last annotation update)			
DE	Guanylate cyclase soluble, alpha-1 chain (EC 4.6.1.2) (GCS-alpha-1)			
DE	(Soluble guanylate cyclase large subunit) (GCS-alpha-3).			
GN	GUCY1A1 OR GUCY1A3 OR GUC1A3 OR GUCSA3.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.			
OX	NCBI_Taxid=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Brain;			
RA	Medline-92316204; PubMed-1352257;			
RT	Guilli G., Scholl U., Bulle F., Guejlaen G.;			
RT	"Molecular cloning of the cDNAs coding for the two subunits of			
RT	soluble guanylyl cyclase from human brain.";			
RL	FEBS Lett. 304:83-86(1992).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Kidney;			
RA	Gansmaes Y., Brockaert P., Fiers M.;			
RT	"Human soluble guanylate cyclase large subunit mRNA, alpha3-like.";			
RT	Submitted (Mar-1996) to the EMBL/Genbank/DBJ databases.			
RL	[3]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Brain;			
RA	Medline-98416113; PubMed-9742212;			
RT	Zabel U., Weeger M., La M., Schmidt H.H.;			
RT	"Human soluble guanylate cyclase: functional expression and revised			
RT	isoenzyme family.";			
RL	Biochem. J. 335:51-57(1998).			
CC	-1- CATALYTIC ACTIVITY: GTP -> 3',5'-cyclic GMP + diphosphate.			
CC	-1- ENZYME REGULATION: ACTIVATED BY NITRIC OXIDE IN THE PRESENCE OF			
CC	MAGNESIUM OR MANGANESE IONS.			
CC	-1- SUBUNIT LOCATION: CYTOPLASMIC.			
CC	-1- MISCELLANEOUS: THERE ARE TWO TYPES OF GUANYLATE CYCLASES: SOLUBLE			
CC	FORMS AND MEMBRANE-ASSOCIATED RECEPTOR FORMS.			
CC	-1- SIMILARITY: BELONGS TO GUANYLYL CYCLASE CLASS-4/GUANYLYL CYCLASE			
CC	FAMILY.			
CC	-----			
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CC	entities requires a license agreement (see http://www.isb-sib.ch/announce/			
CC	or send an email to license@sib-sib.ch).			
CC	-----			
DR	EMBL; X66534; CAA47145.1; -			
DR	EMBL; U58855; AAB94794.1; -			



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OM protein - protein search, using sw model

Run on: June 27, 2003, 12:55:07 ; Search time 9.93048 Seconds  
(without alignments)  
2583.358 Million cell updates/sec

Title: US-09-762-767a-4

Perfect score: 3231

Sequence: 1 MYGFVNALELVIRNYGPE.....QWFLSRKNTGTEETKDDDD 619

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3231	100.0	619	1	CYGL_HUMAN
2	3206	99.2	619	1	CYGL_BOVIN
3	3188	98.7	619	1	CYGL_RAT
4	987	30.5	682	1	CYGL_MOUSE
5	927	28.7	617	1	CYGL_HUMAN
6	916	28.4	730	1	CYGL_RAT
7	909.5	28.1	732	1	CYGL_HUMAN
8	793	24.5	690	1	CYGL_RAT
9	789.5	24.4	690	1	CYGL_HUMAN
10	770	23.8	691	1	CYGL_BOVIN
11	712	22.0	683	1	CYGL_MOUSE
12	481.5	14.9	1061	1	ANPA_HUMAN
13	468	14.5	1057	1	ANPA_RAT
14	466	14.4	1057	1	ANPA_MOUSE
15	454.5	14.1	1047	1	ANPB_HUMAN
16	453.5	14.0	1047	1	ANPB_BOVIN
17	450.5	13.9	1110	1	CYGL_BOVIN
18	438.5	13.6	1110	1	CYGL_MOUSE
19	433.5	13.4	1108	1	CYGL_HUMAN
20	433	13.4	1109	1	CYGL_MOUSE
21	428.5	13.3	1108	1	CYGL_RAT
22	425	13.2	1050	1	CYGL_HUMAN
23	424	13.1	1108	1	CYGL_HUMAN
24	422.5	13.1	1103	1	CYGL_RAT
25	420	13.0	1103	1	CYGL_BOVIN
26	419	13.0	1103	1	CYGL_RAT
27	415.5	12.9	1110	1	CYGL_RAT
28	410	12.7	1137	1	CYGL_MOUSE
29	409	12.7	433	1	HSER_HUMAN
30	405.5	12.6	1073	1	HSER_HUMAN
31	405	12.5	1073	1	HSER_PIG
32	404	12.5	1072	1	HSER_RAT
33	391	12.1	1125	1	CYGL_MOUSE

34	389	12.0	1076	1	HSER_CAVPO
35	345.5	10.7	443	1	CYAL_MYCTU
36	309.5	9.6	1134	1	CYAL_BOVIN
37	308.5	9.5	1248	1	CYAL_RAT
38	302.5	9.4	1251	1	CYAL_HUMAN
39	302.5	9.4	1305	1	CYAL_XENLA
40	301.5	9.3	839	1	CYAL_HUMAN
41	301.5	9.3	1249	1	CYAL_MOUSE
42	300.5	9.3	2248	1	CYAL_MOUSE
43	289	9.3	858	1	CYAL_DICDI
44	283	9.1	1144	1	CYAL_HUMAN
45	292.5	9.1	1334	1	CYAL_CHICK

## ALIGNMENTS

## RESULT 1

ID CYGL\_HUMAN STANDARD: PRT: 619 AA.

AC 002153: 01-JUL-1993 (Rel. 26, Created)  
 DT 01-JUL-1993 (Rel. 26, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Guanylate cyclase soluble, beta-1 chain (EC 4.6.1.2) (CCS-beta-1)  
 DE (soluble guanylate cyclase small subunit) (CCS-beta-3).  
 GN GUCY1B1 OR GUCY1B3 OR GUC1B3 OR GUCS3.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 NX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORM HSGC-2).  
 RC TISSUE=Brain;  
 RX MEDLINE=92316204; PubMed=132257;  
 RA Guilli G., Scholl U., Bulle F., Guejlaen G.;  
 RT Molecular cloning of the cDNAs coding for the two subunits of  
 RL soluble guanylate cyclase from human brain.\*;  
 RL FEBS Lett. 304:83-86(1992).

RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORM HSGC-2).  
 RC TISSUE=Kidney;  
 RA Ganssems T., Brouckaert P., Fiers W.;  
 RL Submitted (Aug-1997) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE OF 337-545, AND ALTERNATIVE SPLICING.  
 RC TISSUE=Lung;  
 RX MEDLINE=92008652; PubMed=1680753;  
 RA Chhajlani V., Friendberg P.-A., Ahlner J., Axelsson K.L.,  
 RA Wikberg J.E.S.;  
 RT Heterogeneity in human soluble guanylate cyclase due to alternative  
 RT splicing.\*;  
 RL FEBS Lett. 290:157-158(1991).

CC -1- CATALYTIC ACTIVITY: GTP -> 3',5'-cyclic GMP + diphosphate.  
 CC -1- ENZYME REGULATION: ACTIVATED BY NITRIC OXIDE IN THE PRESENCE OF  
 CC MAGNESIUM OR MANGANESE IONS.  
 CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.  
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS, HSGC-1 (SHOWN HERE) AND HSGC-2;  
 CC ARE PRODUCED BY ALTERNATIVE SPLICING.  
 CC -1- MISCELLANEOUS: THERE ARE TWO TYPES OF GUANYLATE CYCLASES: SOLUBLE  
 CC FORMS AND MEMBRANE-ASSOCIATED RECEPTOR FORMS.  
 CC -1- SIMILARITY: BELONGS TO GUANYLATE CYCLASE CLASS-4/GUANYLATE CYCLASE  
 CC FAMILY.

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DR EMBL: X65533; CAA7144.1; -  
 DR EMBL: AF020340; MAB94877.1; -  
 DR PIR: S23097; S23097.  
 DR HSSP: P15068; 1AMN.  
 DR Genew: HGNC:4687; GUCY1B3.  
 DR MIM: 139397; -  
 DR InterPro: IPR001054; G\_cyclase.  
 DR Pfam: PF00211; guanylate\_cyc; 1.  
 DR SMART: SM00044; CYC; 1.  
 DR PROSITE: PS00452; GUANYLATE\_CYCLASES\_1; 1.  
 DR PROSITE: PS0125; GUANYLATE\_CYCLASES\_2; 1.  
 DR Lyase: cGMP synthetase; Alternative splicing.  
 FT DOMAIN 421 554 GUANYLATE CYCLASE.  
 FT VARSPLIC 393 425 MISSING (IN ISOFORM HSCG-2).  
 SQ SEQUENCE 619 AA; 70514 MW; 231E4E60DE02AA1 CRC64;

Query Match 100.0%; Score 3231; DB 1; Length 619;  
 Best Local Similarity 100.0%; Pred. No. 2e-215;  
 Matches 619; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGFVNALELLVIRNNGPEWEDIKKEAQDEEGQFLVRIIYDSKTYDLVAASKVTLN 60  
 DB 1 MGFVNALELLVIRNNGPEWEDIKKEAQDEEGQFLVRIIYDSKTYDLVAASKVTLN 60  
 QY 61 LNAEILQMFGRKFFVCOESGYDTILRVLGSNVREFLQNDALHDLATYPGMRAPSF 120  
 DB 61 LNAEILQMFGRKFFVCOESGYDTILRVLGSNVREFLQNDALHDLATYPGMRAPSF 120  
 QY 121 RCTDAKRGKGLIHYSEREGLODIYGIITVAQOIHGTEDIMKRYIQQRNECDHTQFL 180  
 DB 121 RCTDAKRGKGLIHYSEREGLODIYGIITVAQOIHGTEDIMKRYIQQRNECDHTQFL 180  
 QY 121 RCTDAKRGKGLIHYSEREGLODIYGIITVAQOIHGTEDIMKRYIQQRNECDHTQFL 180  
 DB 121 RCTDAKRGKGLIHYSEREGLODIYGIITVAQOIHGTEDIMKRYIQQRNECDHTQFL 180  
 QY 181 IEKESKEDDYEDLDREENGQESRISPTFCAPPPHIFEDRLVYTCGNATRYVL 240  
 DB 181 IEKESKEDDYEDLDREENGQESRISPTFCAPPPHIFEDRLVYTCGNATRYVL 240  
 QY 181 IEKESKEDDYEDLDREENGQESRISPTFCAPPPHIFEDRLVYTCGNATRYVL 240  
 DB 181 IEKESKEDDYEDLDREENGQESRISPTFCAPPPHIFEDRLVYTCGNATRYVL 240  
 QY 241 POLQPGNCSLLSVFSLVPRHIDISPHGISHTNTVFLYLRSEGLLDVEKLECEDELVTGE 300  
 DB 241 POLQPGNCSLLSVFSLVPRHIDISPHGISHTNTVFLYLRSEGLLDVEKLECEDELVTGE 300  
 QY 241 POLQPGNCSLLSVFSLVPRHIDISPHGISHTNTVFLYLRSEGLLDVEKLECEDELVTGE 300  
 DB 241 POLQPGNCSLLSVFSLVPRHIDISPHGISHTNTVFLYLRSEGLLDVEKLECEDELVTGE 300  
 QY 301 ISCLRLKGMKTYLPKADSLIFLCSPSVANLDDLTRRGYLSDIPLDADTRDVLTLGEQR 360  
 DB 301 ISCLRLKGMKTYLPKADSLIFLCSPSVANLDDLTRRGYLSDIPLDADTRDVLTLGEQR 360  
 QY 301 ISCLRLKGMKTYLPKADSLIFLCSPSVANLDDLTRRGYLSDIPLDADTRDVLTLGEQR 360  
 DB 301 ISCLRLKGMKTYLPKADSLIFLCSPSVANLDDLTRRGYLSDIPLDADTRDVLTLGEQR 360  
 QY 361 EEYKIQEELTLDRLQLTLALDEKRTDTLLSYSLPSVANLDRKRPVAKRYDNY 420  
 DB 361 EEYKIQEELTLDRLQLTLALDEKRTDTLLSYSLPSVANLDRKRPVAKRYDNY 420  
 QY 361 EEYKIQEELTLDRLQLTLALDEKRTDTLLSYSLPSVANLDRKRPVAKRYDNY 420  
 DB 361 EEYKIQEELTLDRLQLTLALDEKRTDTLLSYSLPSVANLDRKRPVAKRYDNY 420  
 QY 421 TILPSGIVGFNAFCSHASGEBAKTIYVNLNDLTTRDTLDSKNPFYTKVETVGDKN 480  
 DB 421 TILPSGIVGFNAFCSHASGEBAKTIYVNLNDLTTRDTLDSKNPFYTKVETVGDKN 480  
 QY 421 TILPSGIVGFNAFCSHASGEBAKTIYVNLNDLTTRDTLDSKNPFYTKVETVGDKN 480  
 DB 421 TILPSGIVGFNAFCSHASGEBAKTIYVNLNDLTTRDTLDSKNPFYTKVETVGDKN 480  
 QY 481 TVSGLPSPCIHARSICHLADMEIAGOVQDESVOITGIGTGVTVGVIGQMPRY 540  
 DB 481 TVSGLPSPCIHARSICHLADMEIAGOVQDESVOITGIGTGVTVGVIGQMPRY 540  
 QY 481 TVSGLPSPCIHARSICHLADMEIAGOVQDESVOITGIGTGVTVGVIGQMPRY 540  
 DB 481 TVSGLPSPCIHARSICHLADMEIAGOVQDESVOITGIGTGVTVGVIGQMPRY 540  
 QY 541 CILGNTVNTLSRTETGEGRTVSEGYRCLAMPENDPOPHLEHGPVSMGKREPMQ 600  
 DB 541 CILGNTVNTLSRTETGEGRTVSEGYRCLAMPENDPOPHLEHGPVSMGKREPMQ 600  
 QY 541 CILGNTVNTLSRTETGEGRTVSEGYRCLAMPENDPOPHLEHGPVSMGKREPMQ 600  
 DB 541 CILGNTVNTLSRTETGEGRTVSEGYRCLAMPENDPOPHLEHGPVSMGKREPMQ 600  
 QY 601 VMFLSRKNTGETEKODD 619  
 DB 601 VMFLSRKNTGETEKODD 619

## RESULT 2

AC CYG1\_BOVIN STANDARD; PRT; 619 AA.  
 AC P16068;  
 DT 01-APR-1990 (Rel. 14, Created)  
 DT 01-APR-1990 (Rel. 14, Last sequence update)  
 DT 18-OCT-2001 (Rel. 40, Last annotation update)  
 DE Guanylate cyclase soluble, beta-1 chain (EC 4.6.1.2) (GCS-beta-1)

DE (Soluble guanylate cyclase small subunit).  
 GN GUCY1B1 OR GUCY1B3 OR GUCY1B3.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OC NCBI\_TaxID=9913;  
 RN (1)  
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
 RC TISSUE=Lung;  
 RX MEDLINE=8903114; PubMed=2903071;  
 RA Koenigling D., Herz J., Ganssperl H., Niermann F., Hirsch K.-D.,  
 RA Muelach A., Boehme E., Schultz G., Frank R.;  
 RT "The primary structure of the 70 kDa subunit of bovine soluble  
 RT guanylate cyclase.";  
 RL FEBS Lett. 239:29-34(1988).  
 RN (2)  
 RP 3D-STRUCTURE MODELING OF 412-572.  
 RX MEDLINE=98054247; PubMed=9391039;  
 RA Liu Y., Ruocho A.E., Rao V.D., Hurley J.H.;  
 RT "Catalytic mechanism of the adenylyl and guanylyl cyclases: modeling  
 RT and mutational analysis.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 94:13414-13419(1997).  
 CC -1- CATALYTIC ACTIVITY: GTP -> 3',5'-cyclic GMP + diphosphate.  
 CC -1- ENZYME REGULATION: ACTIVATED BY NITRIC OXIDE IN THE PRESENCE OF  
 CC MAGNESIUM OR MANGANESE IONS.  
 CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- TISSUE SPECIFICITY: LUNG AND BRAIN.  
 CC -1- MISCELLANEOUS: THERE ARE TWO TYPES OF GUANYLATE CYCLASES: SOLUBLE  
 CC -1- FORMS AND MEMBRANE-ASSOCIATED RECEPTOR FORMS.  
 CC -1- SIMILARITY: BELONGS TO ADENYLYL CYCLASE CLASS-4/GUANYLYL CYCLASE  
 CC FAMILY.  
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 DR EMBL: Y00770; CAA68739.1; -  
 DR PIR: S01653; OYB070.  
 DR PDB: 1AMN; 28-JAN-98.  
 DR InterPro: IPR001054; G\_cyclase.  
 DR Pfam: PF00211; guanylate\_cyc; 1.  
 DR SMART: SM00044; CYC; 1.  
 DR PROSITE: PS00452; GUANYLATE\_CYCLASES\_1; 1.  
 DR PROSITE: PS0125; GUANYLATE\_CYCLASES\_2; 1.  
 DR Lyase: cGMP synthetase; 3D-structure.  
 FT DOMAIN 421 554 GUANYLATE CYCLASE.  
 SQ SEQUENCE 619 AA; 70502 MW; 8EF814952880F344 CRC64;

Query Match 99.2%; Score 3206; DB 1; Length 619;  
 Best Local Similarity 99.0%; Pred. No. 1e-213;  
 Matches 613; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGFVNALELLVIRNNGPEWEDIKKEAQDEEGQFLVRIIYDSKTYDLVAASKVTLN 60  
 DB 1 MGFVNALELLVIRNNGPEWEDIKKEAQDEEGQFLVRIIYDSKTYDLVAASKVTLN 60  
 QY 61 LNAEILQMFGRKFFVCOESGYDTILRVLGSNVREFLQNDALHDLATYPGMRAPSF 120  
 DB 61 LNAEILQMFGRKFFVCOESGYDTILRVLGSNVREFLQNDALHDLATYPGMRAPSF 120  
 QY 121 RCTDAKRGKGLIHYSEREGLODIYGIITVAQOIHGTEDIMKRYIQQRNECDHTQFL 180  
 DB 121 RCTDAKRGKGLIHYSEREGLODIYGIITVAQOIHGTEDIMKRYIQQRNECDHTQFL 180  
 QY 121 RCTDAKRGKGLIHYSEREGLODIYGIITVAQOIHGTEDIMKRYIQQRNECDHTQFL 180  
 DB 121 RCTDAKRGKGLIHYSEREGLODIYGIITVAQOIHGTEDIMKRYIQQRNECDHTQFL 180  
 QY 181 IEKESKEDDYEDLDREENGQESRISPTFCAPPPHIFEDRLVYTCGNATRYVL 240  
 DB 181 IEKESKEDDYEDLDREENGQESRISPTFCAPPPHIFEDRLVYTCGNATRYVL 240  
 QY 181 IEKESKEDDYEDLDREENGQESRISPTFCAPPPHIFEDRLVYTCGNATRYVL 240  
 DB 181 IEKESKEDDYEDLDREENGQESRISPTFCAPPPHIFEDRLVYTCGNATRYVL 240